

10/566679

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SEQUENCE LISTING

<110> CNRS

<120> NOVEL ANTI-ANGIOGENIC AGENT AND ITS USE, IN PARTICULAR  
WITHIN THE FRAMEWORK OF THE TREATMENT OF CANCER

<130> 1487-28

<140> Unassigned

<141> 2006-02-01

<150> PCT/FR04/02050

<151> 2004-07-30

<150> FR 03/09506

<151> 2003-08-01

<160> 12

<170> PatentIn version 3.1

<210> 1

<211> 2389

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (73)..(1143)

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111

Met Gln Ser Val Gln Ser Thr Ser Phe Cys Leu Arg Lys  
1 5 10

cag tgc ctt tgc ctg acc ttc ctg ctt ctc cat ctc ctg gga cag gtc  
159

Gln Cys Leu Cys Leu Thr Phe Leu Leu Leu His Leu Leu Gly Gln Val  
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gct gcg act cag cgc tgc cct ccc cag tgc ccg ggc cgg tgc cct gcg  
207

Ala Ala Thr Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala  
30 35 40 45

acg ccg ccg acc tgc gcc ccc ggg gtg cgc gcg gtg ctg gac ggc tgc  
255

Thr Pro Pro Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys  
50 55 60

tca tgc tgt ctg gtg tgt gcc cgc cag cgt ggc gag agc tgc tca gat  
303

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 65 70 75  
 ctg gag cca tgc gac gag agc agt ggc ctc tac tgt gat cgc agc gcg  
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 Leu Glu Pro Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala  
 80 85 90  
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 Asp Pro Ser Asn Gln Thr Gly Ile Cys Thr Ala Val Glu Gly Asp Asn  
 95 100 105  
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 Cys Val Phe Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro  
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 130 135 140  
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 Met Gly Phe Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met  
 225 230 235  
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879

Glu Gln Pro Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys  
255 260 265

tca ctc aaa gcc atc cac ctg cag ttc aag aac tgc acc agc ctg cac  
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Ser Leu Lys Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser Leu His  
270 275 280 285

acc tac aag ccc agg ttc tgt ggg gtc tgc agt gat ggc cgc tgc tgc  
975

Thr Tyr Lys Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys  
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1023

Thr Pro His Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys Ser Pro  
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1071

Gly Gln Ile Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys  
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1119

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1173

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1293

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1353

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1473

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1773

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 Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala Thr Pro Pro  
 35 40 45  
 Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys Ser Cys Cys  
 50 55 60  
 Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro  
 65 70 75 80  
 Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser  
 85 90 95  
 Asn Gln Thr Gly Ile Cys Thr Ala Val Glu Gly Asp Asn Cys Val Phe  
 100 105 110  
 Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro Ser Cys Lys  
 115 120 125  
 Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly Cys Val Pro Arg Cys  
 130 135 140

Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys Pro Ala Pro Arg Lys  
 145 150 155 160  
 Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp Ile Cys Gly Pro Asp  
 165 170 175  
 Glu Glu Asp Ser Leu Gly Gly Leu Thr Leu Ala Ala Tyr Arg Pro Glu  
 180 185 190  
 Ala Thr Leu Gly Val Glu Val Ser Asp Ser Ser Val Asn Cys Ile Glu  
 195 200 205  
 Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly Met Gly Phe  
 210 215 220  
 Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met Leu Lys Gln  
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 Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln Glu Pro Glu Gln Pro  
 245 250 255  
 Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys Ser Leu Lys  
 260 265 270  
 Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser Leu His Thr Tyr Lys  
 275 280 285  
 Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys Thr Pro His  
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 Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys His Thr Asn  
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 96  
 Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys Ser Cys Cys  
 20 25 30

ctg gtg tgt gcc cgc cag cgt ggc gag agc tgc tca gat ctg gag cca  
 144  
 Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro  
 35 40 45

tgc gac gag agc agt ggc ctc tac tgt gat cgc agc gcg gac ccc agc  
 192  
 Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser  
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Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro  
 35 40 45

Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser  
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96  
Gln Pro Ser Cys Lys Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly  
20 25 30  
  
tgt gtg ccc cgc tgt cag ctg gat gtg cta ctg cct gag cct aac tgc  
144  
Cys Val Pro Arg Cys Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys  
35 40 45  
  
cca gct cca aga aaa gtt gag gtg cct gga gag tgc tgt gaa aag tgg  
192  
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50 55 60  
  
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Ile Cys Gly  
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Cys Val Pro Arg Cys Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys  
35 40 45  
  
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Ile Cys Gly  
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atg ggg ttc tcc acc cgg gtc acc aat agg aac cgt caa tgt gag atg  
96  
Met Gly Phe Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met  
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<222> (1)..(225)

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1 5 10 15

aac tgc acc agc ctg cac acc tac aag ccc agg ttc tgt ggg gtc tgc  
96

Asn Cys Thr Ser Leu His Thr Tyr Lys Pro Arg Phe Cys Gly Val Cys  
20 25 30

agt gat ggc cgc tgc tgc act ccc cac aat acc aaa acc atc cag gca  
144

Ser Asp Gly Arg Cys Cys Thr Pro His Asn Thr Lys Thr Ile Gln Ala  
35 40 45

gag ttt cag tgc tcc cca ggg caa ata gtc aag aag cca gtg atg gtc  
192

Glu Phe Gln Cys Ser Pro Gly Gln Ile Val Lys Lys Pro Val Met Val  
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35 40 45

Glu Phe Gln Cys Ser Pro Gly Gln Ile Val Lys Lys Pro Val Met Val

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gtc aac tgc att gaa cag acc aca gag tgg aca gca tgc tcc aag agc
96
Val Asn Cys Ile Glu Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser
20           25           30

tgt ggt atg ggg ttc tcc acc cgg gtc acc aat agg aac cgt caa tgt
144
Cys Gly Met Gly Phe Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys
35           40           45

gag atg ctg aaa cag act cgg ctc tgc atg gtg cgg ccc tgt gaa caa
192
Glu Met Leu Lys Gln Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln
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gag cca gag cag cca aca gat aag aaa gga aaa aag tgt ctc cgc acc
240
Glu Pro Glu Gln Pro Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr
65           70           75           80

aag aag tca ctc aaa gcc atc cac ctg cag ttc aag aac tgc acc agc
288
Lys Lys Ser Leu Lys Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser
85           90           95

ctg cac acc tac aag ccc agg ttc tgt ggg gtc tgc agt gat ggc cgc
336
Leu His Thr Tyr Lys Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg
100          105          110

tgc tgc act ccc cac aat acc aaa acc atc cag gca gag ttt cag tgc
384
Cys Cys Thr Pro His Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys
115          120          125

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tcc cca ggg caa ata gtc aag aag cca gtg atg gtc att ggg acc tgc  
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480

Thr Cys His Thr Asn Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu  
145 150 155 160

ctg gag ctg aag act acc aga ggg aaa atg  
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Leu Glu Leu Lys Thr Thr Arg Gly Lys Met  
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<210> 12

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<212> PRT

<213> Homo sapiens

<400> 12

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35 40 45

Glu Met Leu Lys Gln Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln  
50 55 60

Glu Pro Glu Gln Pro Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr  
65 70 75 80

Lys Lys Ser Leu Lys Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser  
85 90 95

Leu His Thr Tyr Lys Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg  
100 105 110

Cys Cys Thr Pro His Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys  
115 120 125

Ser Pro Gly Gln Ile Val Lys Lys Pro Val Met Val Ile Gly Thr Cys  
130 135 140

Thr Cys His Thr Asn Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu  
145 150 155 160

Leu Glu Leu Lys Thr Thr Arg Gly Lys Met  
165 170